

RAW SEQUENCE LISTING
PATENT APPLICATION US/09/030,061

DATE: 03/10/98
TIME: 10:47:26

INPUT SET: S2912.raw

This Raw Listing contains the General
Information Section and up to the first 5 pages.

SEQUENCE LISTING

1
2
3 (1) General Information:
4
5 (i) APPLICANT: GILLISPIE, Matthew Todd
6 HORWOOD, Nicole Joy
7 UDAGAWA, Nobuyuki
8 KURIMOTO, Masashi
9
10 (ii) TITLE OF INVENTION: OSTEOCLASTGENIC INHIBITORY AGENT
11
12 (iii) NUMBER OF SEQUENCES: 28
13
14 (iv) CORRESPONDENCE ADDRESS:
15 (A) ADDRESSEE: BROWDY AND NEIMARK
16 (B) STREET: 419 Seventh Street, N.W., Suite 300
17 (C) CITY: Washington
18 (D) STATE: D.C.
19 (E) COUNTRY: USA
20 (F) ZIP: 20004
21
22 (v) COMPUTER READABLE FORM:
23 (A) MEDIUM TYPE: Floppy disk
24 (B) COMPUTER: IBM PC compatible
25 (C) OPERATING SYSTEM: PC-DOS/MS-DOS
26 (D) SOFTWARE: Patent In Release #1.0, Version #1.30
27
28 (vi) CURRENT APPLICATION DATA:
29 (A) APPLICATION NUMBER:
30 (B) FILING DATE: 25-FEB-1998
31
32 (vii) PRIOR APPLICATION DATA:
33 (A) APPLICATION NUMBER: JP 55,468/1997
34 (B) FILING DATE: 25-FEB-1997
35
36 (viii) ATTORNEY/AGENT INFORMATION:
37 (A) NAME: BROWDY, Roger L.
38 (B) REGISTRATION NUMBER: 25,618
39 (C) REFERENCE/DOCKET NUMBER: GILLISPIE=1
40
41 (ix) TELECOMMUNICATION INFORMATION:
42 (A) TELEPHONE: (202) 628-5197
43 (B) TELEFAX: (202) 737-3528
44
45 (2) INFORMATION FOR SEQ ID NO: 1:
46

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47 (i)SEQUENCE CHARACTERISTICS:
48 (A)LENGTH: 6 amino acids
49 (B)TYPE: amino acid
50 (D)TOPOLOGY: linear
51 (ii)MOLECULE TYPE: peptide
52
53 (v)FRAGMENT TYPE: internal fragment
54
55
56 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 1:
57
58 Asn Asp Gln Val Leu Phe
59 1 5
60
61 (2) INFORMATION FOR SEQ ID NO: 2:
62
63 (i)SEQUENCE CHARACTERISTICS:
64 (A)LENGTH: 6 amino acids
65 (B)TYPE: amino acid
66 (D)TOPOLOGY: linear
67
68 (ii)MOLECULE TYPE: internal fragment
69
70
71 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 2:
72
73 Phe Glu Asp Met Thr Asp
74 1 5
75
76 (2) INFORMATION FOR SEQ ID NO: 3:
77
78 (i)SEQUENCE CHARACTERISTICS:
79 (A)LENGTH: 7 amino acids
80 (B)TYPE: amino acid
81 (D)TOPOLOGY: linear
82
83 (ii)MOLECULE TYPE: peptide
84
85 (v)FRAGMENT TYPE: internal fragment
86
87 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 3:
88
89 Phe Lys Leu Ile Leu Lys Lys
90 1 5
91
92 (2) INFORMATION FOR SEQ ID NO: 4:
93
94 (i)SEQUENCE CHARACTERISTICS:
95 (A)LENGTH: 5 amino acids
96 (B)TYPE: amino acid
97 (D)TOPOLOGY: linear
98
99 (ii)MOLECULE TYPE: internal fragment

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100
101 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 4:
102
103 Met Tyr Lys Asp Ser
104 1 5
105
106 (2) INFORMATION FOR SEQ ID NO: 5:
107
108 (i)SEQUENCE CHARACTERISTICS:
109 (A)LENGTH: 5 amino acids
110 (B)TYPE: amino acid
111 (D)TOPOLOGY: linear
112
113 (ii)MOLECULE TYPE: internal fragment
114
115 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 5:
116
117 Ser Thr Leu Ser Cys
118 1 5
119
120 (2) INFORMATION FOR SEQ ID NO: 6:
121
122 (i)SEQUENCE CHARACTERISTICS:
123 (A)LENGTH: 157 amino acids
124 (B)TYPE: amino acid
125 (D)TOPOLOGY: linear
126 (ii)MOLECULE TYPE: peptide
127
128 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 6:
129
130 Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
131 1 5 10 15
132 Asp Gln Val Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
133 20 25 30
134 Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
135 35 40 45
136 Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
137 50 55 60
138 Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile
139 65 70 75 80
140 Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
141 85 90 95
142 Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
143 100 105 110
144 Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
145 115 120 125
146 Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
147 130 135 140
148 Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
149 145 150 155
150
151 (2) INFORMATION FOR SEQ ID NO: 7:
152

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153 (i)SEQUENCE CHARACTERISTICS:
154 (A)LENGTH: 157 amino acids
155 (B)TYPE: amino acid
156 (D)TOPOLOGY: linear
157
158 (ii)MOLECULE TYPE: peptide
159
160 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 7:
161
162 Asn Phe Gly Arg Leu His Cys Thr Thr Ala Val Ile Arg Asn Ile Asn
163 1 5 10 15
164 Asp Gln Val Leu Phe Val Asp Lys Arg Gln Pro Val Phe Glu Asp Met
165 20 25 30
166 Thr Asp Ile Asp Gln Ser Ala Ser Glu Pro Gln Thr Arg Leu Ile Ile
167 35 40 45
168 Tyr Met Tyr Lys Asp Ser Glu Val Arg Gly Leu Ala Val Thr Leu Ser
169 50 55 60
170 Val Lys Asp Ser Lys Met Ser Thr Leu Ser Cys Lys Asn Lys Ile Ile
171 65 70 75 80
172 Ser Phe Glu Glu Met Asp Pro Pro Glu Asn Ile Asp Asp Ile Gln Ser
173 85 90 95
174 Asp Leu Ile Phe Phe Gln Lys Arg Val Pro Gly His Asn Lys Met Glu
175 100 105 110
176 Phe Glu Ser Ser Leu Tyr Glu Gly His Phe Leu Ala Cys Gln Lys Glu
177 115 120 125
178 Asp Asp Ala Phe Lys Leu Ile Leu Lys Lys Lys Asp Glu Asn Gly Asp
179 130 135 140
180 Lys Ser Val Met Phe Thr Leu Thr Asn Leu His Gln Ser
181 145 150 155

182
183 (2)INFORMATION FOR SEQ ID NO: 8:
184
185 (i)SEQUENCE CHARACTERISTICS:
186 (A)LENGTH: 471 base pairs
187 (B)TYPE: nucleic acid
188 (C)STRANDEDNESS: double
189 (D)TOPOLOGY: linear
190 (ii)MOLECULE TYPE: cDNA
191
192 (vi)ORIGINAL SOURCE:
193 (A)ORGANISM: human
194 (G)CELL TYPE: liver
195
196 (ix)FEATURE:
197 (A)NAME/KEY: mat peptide
198 (B)LOCATION: 1..471
199 (C)IDENTIFICATION METHOD: E
200
201 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 8:
202

203 TAC TTT GGC AAG CTT GAA TCT AAA TTA TCA GTC ATA AGA AAT TTG AAT 48
204 Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser Val Ile Arg Asn Leu Asn
205 1 5 10 15

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206  GAC CAA GTT CTC TTC ATT GAC CAA GGA AAT CGG CCT CTA TTT GAA GAT      96
207  Asp Gln Val  Leu Phe Ile Asp Gln Gly Asn Arg Pro Leu Phe Glu Asp
208              20              25              30
209  ATG ACT GAT TCT GAC TGT AGA GAT AAT GCA CCC CGG ACC ATA TTT ATT      144
210  Met Thr Asp Ser Asp Cys Arg Asp Asn Ala Pro Arg Thr Ile Phe Ile
211              35              40              45
212  ATA AGT ATG TAT AAA GAT AGC CAG CCT AGA GGT ATG GCT GTA ACT ATC      192
213  Ile Ser Met Tyr Lys Asp Ser Gln Pro Arg Gly Met Ala Val Thr Ile
214              50              55              60
215  TCT GTG AAG TGT GAG AAA ATT TCA ACT CTC TCC TGT GAG AAC AAA ATT      240
216  Ser Val Lys Cys Glu Lys Ile Ser Thr Leu Ser Cys Glu Asn Lys Ile
217              65              70              75              80
218  ATT TCC TTT AAG GAA ATG AAT CCT CCT GAT AAC ATC AAG GAT ACA AAA      288
219  Ile Ser Phe Lys Glu Met Asn Pro Pro Asp Asn Ile Lys Asp Thr Lys
220              85              90              95
221  AGT GAC ATC ATA TTC TTT CAG AGA AGT GTC CCA GGA CAT GAT AAT AAG      336
222  Ser Asp Ile Ile Phe Phe Gln Arg Ser Val Pro Gly His Asp Asn Lys
223              100              105              110
224  ATG CAA TTT GAA TCT TCA TCA TAC GAA GGA TAC TTT CTA GCT TGT GAA      384
225  Met Gln Phe Glu Ser Ser Ser Tyr Glu Gly Tyr Phe Leu Ala Cys Glu
226              115              120              125
227  AAA GAG AGA GAC CTT TTT AAA CTC ATT TTG AAA AAA GAG GAT GAA TTG      432
228  Lys Glu Arg Asp Leu Phe Lys Leu Ile Leu Lys Lys Glu Asp Glu Leu
229              130              135              140
230  GGG GAT AGA TCT ATA ATG TTC ACT GTT CAA AAC GAA GAC      471
231  Gly Asp Arg Ser Ile Met Phe Thr Val Gln Asn Glu Asp
232  145              150              155

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233

234 (2) INFORMATION FOR SEQ ID NO: 9:

235

236 (i)SEQUENCE CHARACTERISTICS:

237 (A)LENGTH: 11 amino acids

238 (B)TYPE: amino acid

239 (D)TOPOLOGY: linear

240

241 (ii)MOLECULE TYPE: peptide

242

243 (v)FRAGMENT TYPE: N-terminal fragment

244

245 (xi)SEQUENCE DESCRIPTION: SEQ ID NO: 9:

246

247 Met Tyr Phe Gly Lys Leu Glu Ser Lys Leu Ser

248 1 5 10

249

250 (2) INFORMATION FOR SEQ ID NO: 10:

251

252 (i)SEQUENCE CHARACTERISTICS:

253 (A)LENGTH: 10 amino acids

254 (B)TYPE: amino acid

255 (D)TOPOLOGY: linear

256

257 (ii)MOLECULE TYPE: peptide

258

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SEQUENCE VERIFICATION REPORT
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Error

Original Text